

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/989,362

1644 #6

DATE: 10/15/98
 TIME: 11:13:58

INPUT SET: S29156.raw

**This Raw Listing contains the General
 Information Section and up to the first 5 pages.**

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Gorman, Daniel M.
 Mattson, Jeanine D.

(ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
 Reagents

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
 (B) STREET: 901 California Avenue
 (C) CITY: Palo Alto
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
 (B) FILING DATE: 12-DEC-1997
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,846
 (B) FILING DATE: 13-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
 (B) REGISTRATION NUMBER: 34,090
 (C) REFERENCE/DOCKET NUMBER: DX0686

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
 (B) TELEFAX: (650)496-1204

(2) INFORMATION FOR SEQ ID NO:1:

--> OK

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/989,362DATE: 10/15/98
TIME: 11:13:59

INPUT SET: S29156.raw

47
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 2191 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
53
54 (ii) MOLECULE TYPE: cDNA
55
56
57 (ix) FEATURE:
58 (A) NAME/KEY: CDS
59 (B) LOCATION: 125..1072
60
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCTG GCCGGGAGTC TGCTCGGCGG 60
65
66 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG 120
67
68 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG 169
69 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
70 1 5 10 15
71
72 GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC 217
73 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
74 20 25 30
75
76 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC 265
77 Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
78 35 40 45
79
80 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC 313
81 Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
82 50 55 60
83
84 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA 361
85 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
86 65 70 75
87
88 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT 409
89 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
90 80 85 90 95
91
92 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA 457
93 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
94 100 105 110
95
96 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG 505
97 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
98 115 120 125
99

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100	AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA	553
101	Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro	
102	130 135 140	
103		
104	GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT	601
105	Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro	
106	145 150 155	
107		
108	GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA	649
109	Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
110	160 165 170 175	
111		
112	TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC	697
113	Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
114	180 185 190	
115		
116	TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT	745
117	Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
118	195 200 205	
119		
120	AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT	793
121	Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
122	210 215 220	
123		
124	CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG	841
125	His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
126	225 230 235	
127		
128	TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG	889
129	Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
130	240 245 250 255	
131		
132	AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT	937
133	Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
134	260 265 270	
135		
136	TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA	985
137	Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
138	275 280 285	
139		
140	ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT	1033
141	Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
142	290 295 300	
143		
144	GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT	1082
145	Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
146	305 310 315	
147		
148	TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGTTTGAAAA CTTCTTAAAA AATGGATGAT	1142
149		
150	GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCACG GTGTATGAAA CTCACAGCCC	1202
151		
152	TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTTCAT	1262

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153
154 GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTC TAAGAATTGA ACCAGATTGG 1322
155
156 GAGAGGTATT CCGATGCTTA TGAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC 1382
157
158 TCTGGGTCTA ACCCTGGAC ATGTGCCACT GAGAACCCTG AAATTAAGAA GATGCCATGT 1442
159
160 CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTTT GAATTGTTAC ATTGCGCTGG 1502
161
162 GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTATATA 1562
163
164 ATGTCTAAAG TTATATTTC AAGTGAATGT TTTCTGTGCA AAGTTTTGTA AATTATATTT 1622
165
166 GTGCTATAGT ATTTGATTCA AAATATTTAA AAATGTCTCA CTGTTGACAT ATTTAATGTT 1682
167
168 TTAAATGTAC AGATGTATTT AACTGGTGCA CTTTGTAATT CCCCTGAAGG TACTCGTAGC 1742
169
170 TAAGGGGGCA GAATACTGTT TCTGGTGACC ACATGTAGTT TATTTCTTTA TTCTTTTAA 1802
171
172 CTTAATAGAG TCTTCAGACT TGTCAAACT ATGCAAGCAA AATAAATAAA TAAAAATAAA 1862
173
174 ATGAATATCT TGAATAATAA GTAGGATGTT GGTCACCAGG TGCCTTTCAA ATTTAGAAGC 1922
175
176 TAATTGACTT TAGGAGCTGA CATAGCCAAA AAGGATACAT AATAGGCTAC TGAAAATCTG 1982
177
178 TCAGGAGTAT TTATGCAATT ATTGAACAGG TGTCTTTTTT TACAAGAGCT ACAAATTGTA 2042
179
180 AATTTTGTTT CTTTTTTTTT CCATAGAAAA TGTACTATAG TTTATCAGCC AAAAAACAAT 2102
181
182 CCACTTTTTA ATTTAGTGAA AGTTATTTTA TTATACTGTA CAATAAAAGC ATTGTTTCTG 2162
183
184 AATGGCATT TTTGGTACTT AAAAATGGC 2191
185
186

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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198 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
199   1           5           10           15
200
201 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
202           20           25           30
203
204 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
205           35           40           45

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206																	
207	Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	
208		50					55					60					
209																	
210	Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	
211	65					70					75					80	
212																	
213	Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	
214					85					90					95		
215																	
216	Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	
217				100					105					110			
218																	
219	Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	
220			115					120					125				
221																	
222	Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	
223		130					135					140					
224																	
225	Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	
226	145					150					155					160	
227																	
228	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	
229					165					170					175		
230																	
231	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	
232				180					185					190			
233																	
234	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	
235			195					200					205				
236																	
237	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	
238		210					215					220					
239																	
240	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	
241	225					230					235					240	
242																	
243	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	
244					245					250					255		
245																	
246	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	
247				260					265					270			
248																	

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/989,362

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Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US